

RAW SEQUENCE LISTING

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Application Serial Number: 08/252,384 c
Source: IFW16
Date Processed by STIC: 11/10/2005

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IFW/b

RAW SEQUENCE LISTING

DATE: 11/10/2005

PATENT APPLICATION: US/08/252,384C

TIME: 12:22:35

Input Set : A:\seq listing.txt

Output Set: N:\CRF4\11102005\H252384C.raw

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3 <110> APPLICANT: Reactive Surfaces, Ltd.
4     McDaniel, Steven
5     Raushel, Frank M
6     Wild, James R
8 <120> TITLE OF INVENTION: Recombinant Organophosphorous Acid Anhydrase and Methods of Use
10 <130> FILE REFERENCE: TAMK145
12 <140> CURRENT APPLICATION NUMBER: US 08/252,384C
13 <141> CURRENT FILING DATE: 1994-06-01
15 <150> PRIOR APPLICATION NUMBER: US 07/928,540
16 <151> PRIOR FILING DATE: 1992-08-13
18 <150> PRIOR APPLICATION NUMBER: US 07/344,258
19 <151> PRIOR FILING DATE: 1989-04-27
21 <160> NUMBER OF SEQ ID NOS: 2
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1337
27 <212> TYPE: DNA
28 <213> ORGANISM: Pseudomonas diminuta
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (63)..(1160)
35 <400> SEQUENCE: 1
36 ctgcagcctg actcggcacc agtcgctgca agcagagtcg taagcaatcg caaggggggca      60
38 gc atg caa acg aga agg gtt gtg ctc aag tct gcg gcc gcc gca gga      107
39   Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Ala Gly
40   1           5           10           15
42 act ctg ctc ggc ggc ctg gct ggg tgc gcg agc gtg gct gga tcg atc      155
43 Thr Leu Leu Gly Gly Leu Ala Gly Cys Ala Ser Val Ala Gly Ser Ile
44           20           25           30
46 ggc aca ggc gat cgg atc aat acc gtg cgc ggt cct atc aca atc tct      203
47 Gly Thr Gly Asp Arg Ile Asn Thr Val Arg Gly Pro Ile Thr Ile Ser
48           35           40           45
50 gaa gcg ggt ttc aca ctg act cac gag cac atc tgc ggc agc tcg gca      251
51 Glu Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly Ser Ser Ala
52           50           55           60
54 gga ttc ttg cgt gct tgg cca gag ttc ttc ggt agc cgc aaa gct cta      299
55 Gly Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu
56           65           70           75
58 gcg gaa aag gct gtg aga gga ttg cgc cgc gcc aga gcg gct ggc gtg      347
59 Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala Ala Gly Val
60 80           85           90           95
62 cga acg att gtc gat gtg tcg act ttc gat atc ggt cgc gac gtc agt      395
63 Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser

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64		100		105		110		
66	tta ttg gcc gag gtt tcg cgg gct gcc gac gtt cat atc gtg gcg gcg							443
67	Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala							
68		115		120		125		
70	acc ggc ttg tgg ttc gac ccg cca ctt tcg atg cga ttg agg agt gta							491
71	Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val							
72		130		135		140		
74	gag gaa ctc aca cag ttc ttc ctg cgt gag att caa tat ggc atc gaa							539
75	Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu							
76		145		150		155		
78	gac acc gga att agg gcg ggc att atc aag gtc gcg acc aca ggc aag							587
79	Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys							
80	160		165		170		175	
82	gcg acc ccc ttt cag gag tta gtg tta aag gcg gcc gcc ccg gcc agc							635
83	Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser							
84		180		185		190		
86	ttg gcc acc ggt gtt ccg gta acc act cac acg gca gca agt cag cgc							683
87	Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser Gln Arg							
88		195		200		205		
90	gat ggt gag cag cag gcc gcc att ttt gag tcc gaa ggc ttg agc ccc							731
91	Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly Leu Ser Pro							
92		210		215		220		
94	tca cgg gtt tgt att ggt cac agc gat gat act gac gat ttg agc tat							779
95	Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp Leu Ser Tyr							
96		225		230		235		
98	ctc acc gcc ctc gct gcg cgc gga tac ctc atc ggt cta gac cac atc							827
99	Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile							
100	240		245		250		255	
102	ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca tca gcc ctc							875
103	Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu							
104		260		265		270		
106	ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc aag gcg ctc							923
107	Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu							
108		275		280		285		
110	atc gac caa ggc tac atg aaa caa atc ctc gtt tcg aat gac tgg ctg							971
111	Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu							
112		290		295		300		
114	ttc ggg ttt tcg agc tat gtc acc aac atc atg gac gtg atg gat cgc							1019
115	Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg							
116		305		310		315		
118	gtg aac ccc gac ggg atg gcc ttc att cca ctg aga gtg atc cca ttc							1067
119	Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe							
120	320		325		330		335	
122	cta cga gag aag ggc gtc cca cag gaa acg ctg gca ggc atc act gtg							1115
123	Leu Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly Ile Thr Val							
124		340		345		350		
126	act aac ccg gcg ccg ttc ttg tca ccg acc ttg ccg gcg tca tga							1160
127	Thr Asn Pro Ala Arg Phe Leu Ser Pro Thr Leu Arg Ala Ser							
128		355		360		365		

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130 cgccatctgg atccttccag ccagcggcca ctattccccg tcaagatacc gaacgatgaa 1220
132 gtcgcgcata gatcgatagg catcttcaat ttgatcaggg ctgccacctc caaagccgtg 1280
134 gccacccttg tcgatagtct tgaggacgta gggcacaccg tgcttttcga actgcag 1337
137 <210> SEQ ID NO: 2
138 <211> LENGTH: 365
139 <212> TYPE: PRT
140 <213> ORGANISM: Pseudomonas diminuta
142 <400> SEQUENCE: 2
144 Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Ala Gly Thr
145 1 5 10 15
148 Leu Leu Gly Gly Leu Ala Gly Cys Ala Ser Val Ala Gly Ser Ile Gly
149 20 25 30
152 Thr Gly Asp Arg Ile Asn Thr Val Arg Gly Pro Ile Thr Ile Ser Glu
153 35 40 45
156 Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly Ser Ser Ala Gly
157 50 55 60
160 Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu Ala
161 65 70 75 80
164 Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala Ala Gly Val Arg
165 85 90 95
168 Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser Leu
169 100 105 110
172 Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala Thr
173 115 120 125
176 Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val Glu
177 130 135 140
180 Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu Asp
181 145 150 155 160
184 Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys Ala
185 165 170 175
188 Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu
189 180 185 190
192 Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser Gln Arg Asp
193 195 200 205
196 Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly Leu Ser Pro Ser
197 210 215 220
200 Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp Leu Ser Tyr Leu
201 225 230 235 240
204 Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro
205 245 250 255
208 His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu Leu
209 260 265 270
212 Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile
213 275 280 285
216 Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu Phe
217 290 295 300
220 Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val
221 305 310 315 320
224 Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe Leu

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225					325					330					335	
228	Arg	Glu	Lys	Gly	Val	Pro	Gln	Glu	Thr	Leu	Ala	Gly	Ile	Thr	Val	Thr
229				340					345					350		
232	Asn	Pro	Ala	Arg	Phe	Leu	Ser	Pro	Thr	Leu	Arg	Ala	Ser			
233			355					360					365			

VERIFICATION SUMMARY

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